



SEQUENCE LISTING

#6

<110>Medlock et al.

<120> IL-17 Receptor Like Molecules and Uses Thereof

<130> 01017/36917A

<140> US 09/810,927

<141> 2001-03-16

<150> US 60/266,159

<151> 2001-02-02

<150> US 09/723,232

<151> 2000-11-27

<150> US 60/204,208

<151> 2000-05-12

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<170> PatentIn Ver. 2.0

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 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
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 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
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 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
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 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
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 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
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 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
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 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
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Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
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 370 375 380
 Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
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 405 410 415
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 Gly Cys Cys Arg His Gln Val Gln Ile Gln Pro Phe Phe Ser Ser Cys
 225 230 235 240
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 Trp Phe Ile Thr Gly Ile Ser Ile Leu Leu Val Gly Ser Val Ile Leu
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 Met His Arg Val Gly Glu Leu Ser Gly Asp Asn Tyr Leu Arg Ser Pro
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Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr	
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Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr	
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ccc ctg gga aac aga tac atg gct ctt atc caa cac agc act atc atc	874
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485 490 495

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Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr
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Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly
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 Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu
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 Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile
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 His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr Lys
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Ile Pro Asn Ala Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn		
	25 30 35	
ttc acc tca cca ggc tgc cta gac cac ata atg aaa tat aaa aaa aag	437	
Phe Thr Ser Pro Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys		
	40 45 50 55	
tgt gtc aag gcc gga agc ctg tgg gat ccg aac atc act gct tgt aag	485	
Cys Val Lys Ala Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys		
	60 65 70	
aag aat gag gag aca gta gaa gtg aac ttc aca acc act ccc ctg gga	533	
Lys Asn Glu Glu Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly		
	75 80 85	
aac aga tac atg gct ctt atc caa cac agc act atc atc ggg ttt tct	581	
Asn Arg Tyr Met Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser		
	90 95 100	
cag gtg ttt gag cca cac cag aag aaa caa acg cga gct tca gtg gtg	629	
Gln Val Phe Glu Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val		
	105 110 115	
att cca gtg act ggg gat agt gaa ggt gct acg gtg cag ctg act cca	677	
Ile Pro Val Thr Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro		
	120 125 130 135	
tat ttt cct act tgt ggc agc gac tgc atc cga cat aaa gga aca gtt	725	
Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val		
	140 145 150	
gtg ctg tgc cca caa aca ggc gtc cct ttc cct ctg gat aac aac aaa	773	
Val Leu Cys Pro Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys		
	155 160 165	
agc aag ccg gga ggc tgg ctg cct ctg ctg ctg ctg tct ctg ctg gtg	821	
Ser Lys Pro Gly Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val		
	170 175 180	
gcc aca tgg gtg ctg gtg gca ggg atc tat cta atg tgg agg cac gaa	869	
Ala Thr Trp Val Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu		
	185 190 195	
agg atc aag aag act tcc ttt tct acc acc aca cta ctg ccc ccc att	917	
Arg Ile Lys Lys Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile		
	200 205 210 215	
aag gtt ctt gtg gtt tac cca tct gaa ata tgt ttc cat cac aca att	965	
Lys Val Leu Val Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile		
	220 225 230	

tgt tac ttc act gaa ttt ctt caa aac cat tgc aga agt gag gtc atc	1013
Cys Tyr Phe Thr Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile	
235 240 245	
ctc gaa aag tgg cag aaa aag aaa ata gca gag atg ggt cca gtg cag	1061
Leu Glu Lys Trp Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln	
250 255 260	
tgg ctt gcc act caa aag aag gca gca gac aaa gtc gtc ttc ctt ctt	1109
Trp Leu Ala Thr Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu	
265 270 275	
tcc aat gac gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag	1157
Ser Asn Asp Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu	
280 285 290 295	
ggc agt ccc agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac	1205
Gly Ser Pro Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn	
300 305 310	
ctt ttc tgc agt gat cta aga agc cag att cat ctg cac aaa tac gtg	1253
Leu Phe Cys Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val	
315 320 325	
gtg gtc tac ttt aga gag att gat aca aaa gac gat tac aat gct ctc	1301
Val Val Tyr Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu	
330 335 340	
agt gtc tgc ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt	1349
Ser Val Cys Pro Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys	
345 350 355	
gca gaa ctt ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca	1397
Ala Glu Leu Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser	
360 365 370 375	
caa gcc tgc cac gat ggc tgc tgc tcc ttg tagccccaccc atgagaagca	1447
Gln Ala Cys His Asp Gly Cys Cys Ser Leu	
380 385	
agagacctta aaggcttccct atcccaccaa ttacaggggaa aaaacgtgtg atgatacctga	1507
agcttactat gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaatt	1567
ttcaaatatt gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc	1627
aaagctgttt tatacataga aatcaattac agctttaatt gaaaactgta accattttga	1687
taatgcaaca ataaagcatc ttcagc	1713
<210> 7	
<211> 385	
<212> PRT	
<213> Homo sapiens	
<400> 7	
Met Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val	
1 5 10 15	



Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp
20 25 30
Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His
35 40 45
Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp
50 55 60
Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn
65 70 75 80
Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His
85 90 95
Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys
100 105 110
Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly
115 120 125
Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys
130 135 140
Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro
145 150 155 160
Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Leu
165 170 175
Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val Leu Val Ala Gly Ile
180 185 190
Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys Thr Ser Phe Ser Thr
195 200 205
Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val Val Tyr Pro Ser Glu
210 215 220
Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr Glu Phe Leu Gln Asn
225 230 235 240
His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp Gln Lys Lys Lys Ile
245 250 255
Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr Gln Lys Lys Ala Ala
260 265 270
Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val Asn Ser Val Cys Asp
275 280 285
Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser Glu Asn Ser Gln Asp
290 295 300
Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser Asp Leu Arg Ser Gln
305 310 315 320
Ile His Leu His Lys Tyr Val Val Val Tyr Phe Arg Glu Ile Asp Thr
325 330 335
Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro Lys Tyr His Leu Met
340 345 350

Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu His Val Lys Gln Gln
355 360 365

Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His Asp Gly Cys Cys Ser
370 375 380

Leu
385

<210> 8
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
2429-59

<400> 8
gcagacactg agagcattgt aatcg 25

<210> 9
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
1916-83

<400> 9
ggctcgtatg ttgtgtggaa ttgtgag 27

<210> 10
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
2429-56

<400> 10
atcaagaaga cttccttttc tac 23

<210> 11
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer 1916-80

<400> 11
tgcaaggcga ttaagttggg taacgccag 29

<210> 12
<211> 22

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nested PCR
Primer

<400> 12
gccgacgggg acgtggatga ac 22

<210> 13
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nested PCR
Primer

<400> 13
catgattacg ccaagctcta atacgactc 29

<210> 14
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nested PCR
Primer

<400> 14
cttcgccgag tgctgtgca g 21

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nest PCR
Primer

<400> 15
tcacgacgtt gtaaaacgac ggccagtg 28

<210> 16
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR PRIMER
2469-50

<400> 16
gcgatgtcgc tcgtgctgct aag 23

<210> 17
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PCR Primer
2469-54

<400> 17
gcagcctggt gaggtgaaat tcac

24 ..

<210> 18
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 18
Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg
1 5 10

<210> 19
<211> 18
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peptide

<400> 19
Phe Ile Thr Cys Gly Gly Gly Tyr Gly Arg Lys Lys Arg Arg Gln Arg
1 5 10 15

Arg Arg

<210> 20
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Epogen signal
peptide

<400> 20
Met Gly Val His Glu Cys Pro Ala Trp Leu Trp Leu Leu Leu Ser Leu
1 5 10 15

Leu Ser Leu Pro Leu Gly Leu Pro Val Leu Gly
20 25

<210> 21
<211> 233
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: peptide of Fc
fragment

<400> 21

Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160
Asp Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
165 170 175
Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
180 185 190
Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
195 200 205
Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
210 215 220
Lys Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 22

<211> 644

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (159)..(641)

<400> 22

ctcaagtcac tcctataaaa gacagtggaa ataaatttga ataaacaaaa caggcttgct 60

gaaaataaaa tcaggactcc taacctgctc cagtcagcct gcttccacga ggcctgtcag 120

tcagtgcgcc acttggtgact gagtgtgcag tgcccagc atg tac cag gtg gtt gca 176
Met Tyr Gln Val Val Ala
1 5

ttc ttg gca atg gtc atg gga acc cac acc tac agc cac tgg ccc agc 224
Phe Leu Ala Met Val Met Gly Thr His Thr Tyr Ser His Trp Pro Ser
10 15 20

tgc tgc ccc agc aaa ggg cag gac acc tct gag gag ctg ctg agg tgg 272
Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser Glu Glu Leu Leu Arg Trp
25 30 35

agc act gtg cct gtg cct ccc cta gag cct gct agg ccc aac cgc cac 320
Ser Thr Val Pro Val Pro Pro Leu Glu Pro Ala Arg Pro Asn Arg His
40 45 50

cca gag tcc tgt agg gcc agt gaa gat gga ccc ctc aac agc agg gcc 368
Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly Pro Leu Asn Ser Arg Ala
55 60 65 70

atc tcc ccc tgg aga tat gag ttg gac aga gac ttg aac cgg ctc ccc 416
Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg Asp Leu Asn Arg Leu Pro
75 80 85

cag gac ctg tac cac gcc cgt tgc ctg tgc ccg cac tgc gtc agc cta 464
Gln Asp Leu Tyr His Ala Arg Cys Leu Cys Pro His Cys Val Ser Leu
90 95 100

cag aca ggc tcc cac atg gac ccc cgg ggc aac tcg gag ctg ctc tac 512
Gln Thr Gly Ser His Met Asp Pro Arg Gly Asn Ser Glu Leu Leu Tyr
105 110 115

cac aac cag act gtc ttc tac cgg cgg cca tgc cat ggc gag aag ggc 560
His Asn Gln Thr Val Phe Tyr Arg Arg Pro Cys His Gly Glu Lys Gly
120 125 130

acc cac aag ggc tac tgc ctg gag cgc agg ctg tac cgt gtt tcc tta 608
Thr His Lys Gly Tyr Cys Leu Glu Arg Arg Leu Tyr Arg Val Ser Leu
135 140 145 150

gct tgt gtg tgt gtg cgg ccc cgt gtg atg ggc tag 644
Ala Cys Val Cys Val Arg Pro Arg Val Met Gly
155 160

<210> 23
<211> 161
<212> PRT
<213> Homo sapiens

<400> 23
Met Tyr Gln Val Val Ala Phe Leu Ala Met Val Met Gly Thr His Thr
1 5 10 15
Tyr Ser His Trp Pro Ser Cys Cys Pro Ser Lys Gly Gln Asp Thr Ser
20 25 30
Glu Glu Leu Leu Arg Trp Ser Thr Val Pro Val Pro Pro Leu Glu Pro
35 40 45

Ala Arg Pro Asn Arg His Pro Glu Ser Cys Arg Ala Ser Glu Asp Gly
 50 55 60
 Pro Leu Asn Ser Arg Ala Ile Ser Pro Trp Arg Tyr Glu Leu Asp Arg
 65 70 75 80
 Asp Leu Asn Arg Leu Pro Gln Asp Leu Tyr His Ala Arg Cys Leu Cys
 85 90 95
 Pro His Cys Val Ser Leu Gln Thr Gly Ser His Met Asp Pro Arg Gly
 100 105 110
 Asn Ser Glu Leu Leu Tyr His Asn Gln Thr Val Phe Tyr Arg Arg Pro
 115 120 125
 Cys His Gly Glu Lys Gly Thr His Lys Gly Tyr Cys Leu Glu Arg Arg
 130 135 140
 Leu Tyr Arg Val Ser Leu Ala Cys Val Cys Val Arg Pro Arg Val Met
 145 150 155 160
 Gly

<210> 24
 <211> 521
 <212> PRT
 <213> Homo sapiens

<400> 24
 Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
 1 5 10 15
 Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
 20 25 30
 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
 35 40 45
 Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
 50 55 60
 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
 65 70 75 80
 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
 85 90 95
 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Ser
 100 105 110
 Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn
 115 120 125
 Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn
 130 135 140
 Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu
 145 150 155 160
 Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu
 165 170 175

Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu
 180 185 190
 Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile
 195 200 205
 Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln
 210 215 220
 Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser
 225 230 235 240
 Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser
 245 250 255
 Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly
 260 265 270
 Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu
 275 280 285
 Pro Ala Ala Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
 290 295 300
 Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe
 305 310 315 320
 Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
 325 330 335
 Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
 340 345 350
 Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
 355 360 365
 Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
 370 375 380
 Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
 385 390 395 400
 Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
 405 410 415
 Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
 420 425 430
 Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
 435 440 445
 Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
 450 455 460
 Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
 465 470 475 480
 Phe Phe Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 485 490 495
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 500 505 510

Lys Ser Leu Ser Leu Ser Pro Gly Lys
515 520

<210> 25
<211> 585
<212> PRT
<213> Homo sapiens

<400> 25
Met Ser Leu Val Leu Leu Ser Leu Ala Ala Leu Cys Arg Ser Ala Val
1 5 10 15
Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser Pro
20 25 30
Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
35 40 45
Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
50 55 60
Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
65 70 75 80
Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
85 90 95
Tyr Ser Cys Val Arg Leu Glu Cys Ser Gly Ala Ile Met Ala Arg Cys
100 105 110
Asp Leu Asn Leu Leu Gly Ser Ser Asp Arg Ser Ala Ser Ala Ser Arg
115 120 125
Ala Ala Gly Thr Ala Gly Val Gly His Gln Thr Trp Leu Ile Phe Val
130 135 140
Val Phe Val Glu Gly Gly Phe Thr Val Leu Leu Val Leu Asn Ser Ser
145 150 155 160
Ala Gln Ala Ile Cys Leu Pro Arg Leu Pro Lys Val Leu Gly Leu Gln
165 170 175
Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val Glu Leu Asn Thr Val Tyr
180 185 190
Phe Ile Gly Ala His Asn Ile Pro Asn Ala Asn Met Asn Glu Asp Gly
195 200 205
Pro Ser Met Ser Val Asn Phe Thr Ser Pro Gly Cys Leu Asp His Ile
210 215 220
Met Lys Tyr Lys Lys Lys Cys Val Lys Ala Gly Ser Leu Trp Asp Pro
225 230 235 240
Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu Thr Val Glu Val Asn Phe
245 250 255
Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met Ala Leu Ile Gln His Ser
260 265 270
Thr Ile Ile Gly Phe Ser Gln Val Phe Glu Pro His Gln Lys Lys Gln
275 280 285

Thr Arg Ala Ser Val Val Ile Pro Val Thr Gly Asp Ser Glu Gly Ala
 290 295 300
 Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr Cys Gly Ser Asp Cys Ile
 305 310 315 320
 Arg His Lys Gly Thr Val Val Leu Cys Pro Gln Thr Gly Val Pro Phe
 325 330 335
 Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly Gly Trp Leu Pro Ala Ala
 340 345 350
 Ala Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
 355 360 365
 Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
 370 375 380
 Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
 385 390 395 400
 Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
 405 410 415
 Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
 420 425 430
 Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
 435 440 445
 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
 450 455 460
 Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
 465 470 475 480
 Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
 485 490 495
 Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
 500 505 510
 Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
 515 520 525
 Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
 530 535 540
 Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
 545 550 555 560
 Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
 565 570 575
 Lys Ser Leu Ser Leu Ser Pro Gly Lys
 580 585

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 26

cattttccta catcggttc cctg

24

<210> 27

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR Primer

<400> 27

tgaatctggc ttctttcact gc

22